

CCACACCCTT GEAGAGGIGG GGGTGCTTGA GTGGGTTGCT ANAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG 1 GCTGTGGGAA CCTCTCCACG GGCACGAAGT CASCCAAGGA TITTTTGTAA AITTTTGGGA GTITGACAG AGATGCAAGG GGTGAAGGAG

101 CSTRAGGAA CICTGGGGAC AGAGGGCCCC GGCGGCCTGA IGGCGGAGGC AGGGIGCGAC CCAGGACCCA GGAGGGGTC GGGAACCATA CCAIGGCCG GCHAICECTT GAGACCECTG TETGSCGGGG CEGGEGGAET ACCEGTECG TECCACGETG GGTECTGGGT CETGCEGAG CECTTGGTAT GGTACEGGGE 201 GATCCCCAAG ACCTAAAGT TCSTCSTOST CATCSTOSG STCCTSCTSC CAGTCCTAGG TTACTCTSCC ACCAGGOCG GGCAGGAGGA AGITCCCCAG TEGRATICA AGAGCAGCA GINGCAGCGC CAGGACGACG GICAGGAICG NAIGAGACGG IGGIGACGGG COGICCICCI ICAAGGGGTC

Cluminvala laprogingi ncinarghis SerPhelysG lyGluGluCy sProalacly SerHisargs erGlunisTh rClyalacys AsnProCysThr TENCICCETS TEGRAETICS SECTECTERS AGGICGICET AGAGIATETA GICTIGIATG ACCICGGACA ITGGGCACGI GTCTGTCACC GGGGTGTCGT

CAGAGGGIGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGIT CCTGCACCAT STETECEACA CETAATETEG TEGGBAGGT TETTACTISG AAGAACGAAG GETACATETE AAACATTIAG TETAGITATI GRANTITICAA GGACGIGGIA 401

Gluclyva laspryrthr AsnalaSera snasnGluPr oSerCysPhe ProcysThrv alcysLysSe raspGlnLys HisLysSers erCysThrMet

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAC ACAATGAAA GITCAGICAT TAACAIGCAG GACCCIACIA TAGGICACAC AACIICITAA ACCACGGITA CGGIGACACC ITTGGGGICG AGGACTICIC IGTIACITGI

GinValsera sncysthrse rixpAspAsp ileGincysV alGluGluPh eGlyAlaAsn AlathrValG luthrProAl aAlaGluGlu ThiMetAsnThr 137

Serprocl yThrprohla Prohlahlag lugluthrMe thanThrSer ProGlyThrP rohlaprohl ahlagluglu ThrMetThrT hrSerProGly GSICGGCCC CIGAGGACGG GSICGACGAC TICICTGTA CITGIGGICG GGICCCIGAG GACGGGGTCG AGGACTICIC TGTIACHGGI GGICGGGCCC 701 CCAGCGGGG GACTCCTGCC CCAGCTGCTG AAGAGAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA

171

Ileprolys Thrieulysp heValValVa lileValAla ValLeuLeup roValLeuAl aryrserAla ThrihrAlaA rgGlnGluGl uValProGln

301 CAGACAGEG CCCCACAGCA ACAGAGGCAC AGCITCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA

CHOSTERIOTO TOTCHORONG TOACHTHOOT TECOTGOING GCCTTHOOTH TORGOGGGTOT CTACACGGGC TTCACHTCOT COACGGGAIC ACCCCTTAGA THARTAGAS THYALOYSG INCYSLYSGI UGLYTHTPHE AIGAGANGIUA SHSETPIOGI UNELCYSARG IYSCYSSERA IGCYSPROSE RGIYGIUMELI

FIG._1A-1

- ThrProala Proalaalas lusluthrMe tThrThrser ProslythrP roalaProal aalasluslu ThrMetthrT hrserProsl yThrProala 801 GACTOCINGO COAGCINGIS AAGAGACAAT GACCACCAGG COGGGACTO CTGCCCCAGO TGCTGAAGAG ACAATGACGA COAGCOCGGG GACTOCTGCC CIGAGANCS GGICGANCAN TICICIGIA CIGGIGGICG GGCCCCIGAG GANGGGGICG ANGANTICIC ISTUANIGIGI GGICGGGCCC CIGAGGANGG 204
- ICITOICATI ACCICICAIS CACCAIGGIA GEGAICAIAG ITCIAATIGI GCTICIGATI GIGITIGIII GAAAGACIIC ACIGISGAAG AAAITCCIIC agangagtaa tsgagastac stgstaggat coctagtate aacattaaca cgaagactaa cacaaacaaa cittetgaag tgacacotte titaaggaag SerSerHisT yrLeuSerCy sThrileVal GlyileileV alLeuIleVa lLeuLeuIle ValPheVal 237 901
- SANTGARCIT ICCAAGICCA ICCGCGACCG ACICCCGCCC CCCGCGACCI GIGAGAGACG GGACGGAGGG AGACGACAA AGGIGICIG ICITIGCGGA 1001 CTRCCEGRA RGFTCRGGT AGCCGCTGCC TGAGGCCGGG GGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC AGAAAGGCCT
- CGGGGACGG GITTIMTET TITETITI TYTTITT FYTTWYTTR TITTWYTYF INTRITIT TITTATIT 1101 GCCCTGCCC CARARARARA AARARARARA ARARARARA AARARARARA AARARARARA AARARARARA AARARARARA

FIG._ 1A-2

2/16

- MetGlnGl yValLysGlu ArgPheLeuPro CGACACCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG 1 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
- Leuglyas nserglyasp argalaproa rgProproas pglyarggly argvalargp roargthrol naspglyval glyasnHisT hrmetalaarg 101 CETTAGGAA CICTGGGGAC AGAGGGCCCC GGCGGCCTGA TGGCCGAGGC AGGGTGCGAC CCAGGACCA GGACGGGGC GGAAACATA CCATGGCCCG GDANCCCTT GAGACCCTG TCTCGCGGGG CCGGCGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCGGAG CCCTTGGTAT GGTACCGGGC
- 201 GAYCCCCAAG ACCTAAAGT TCGTGGTGGT CATGGTGGGG GTCCTGGTGC CAGTCCTAGC TTACTGTGGC ACCACTGGCG GGCAGGAGGA AGTTCCCCAG CHAGGGGITC IGGGAITHTA AGCAGCAGCA GIAGCAGCAC CAGGACGACG GICAGGAICG AAIGAGACGG IGGIGACGGG CCGICCICCI ICAAGGGGIC lleprobys Thrieubysp hevalvalva lilevalala Valieuieup rovalieual afyrserala Thrfhralaa rgGlnGluGl uvalProGln
- GINTHIVAJA JAPIOGINGI NGINAKGHIS SEIPHELYSG IYGLUGLUCY SPIOALAGLY SEIHISAKGS EKGIUHISTH KGIYALACYS ASNPIOCYSTHI 301 CAGACAGGG CCCCACAGCA ACAGAGGGAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCTGA CICTOTORCO GGGGTGTCGT TGTCTCCGTG TCGAAGTTCC CCCTCCTCA AGGTCGTCCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT

FIG._ 1B-1

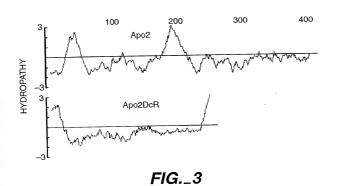
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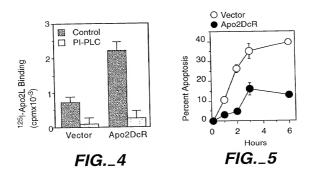
CIGCACCAT	GGACGTGGTA	CHURCHARGIGG TIGGGAAGGI IGTIACTIGG AAGAACGAAG GGIACAAGGA GAGAACGAAG GAGAACGAAGA AAAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	7. CINCHAR DampurThr AsnalaSerA snasnGlupr oSerCysPhe ProCysThrV alcysLysbe Lasperings minglocated
CATAAAAGTT	GTATTTCAA	Tiel vestors	a contracti
AGATCAAAA	TOTACPPTT	27 20 20 40	THEFORETTE
TTTGTAAATC		ייייייייייייייייייייייייייייייייייייייי	alcyshysse
CCATGTACAG	טשטשעט נשטט	COLUCATOR C	ProCysThrV
	212011711	AAGAACGAAG	oSerCysPhe
00 4400 440	ACAMIGMACC	TGTTACTTGG	snAsnGluPr
	MACGCITCCA	TIGCGAAGGI	AsnAlaSerA
	GGATTACACC	CCTAATGTGG	1 aspTvrThr
	CAGAGGGTGT	CTCTCCACA	TO TO TO TAKE
	401		5

- CTSSICICIS TSICACACAG ICACAITICI ICCGIBGAAG SCCITACITI TGASGSGICI CIACACGSCC ITCACAICSI CCACGGGAIC ACCCCIICAS Thrangasp ThrvalcysG lnCysLysGl uGlyThrPhe ArgaanGlua snSerProGl uMetCysArg LysCysSera rgCysProSe rGlyGluVal SOI GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC
- 137 GlnValSera snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr 601 CAAGTCAGTA ATTGIACGIC CTGGGAIGAI AICCAGIGIG ITGAAGAATI TGGIGCCAAI GCCACTGIGG AAACCCCAGC IGGIGAAGAG ACAAIGAACA GITCAGICAI IAACAIGCAG GACCTACIA IAGGICAACA AACITCITAA ACCACGGITA GGGIGACACC ITIGGGGICG ACGACITCIC IGIIACTIGI
- 3 ythrprokla ProklaklaG luGluthrMe tAsnThrSer ProGlythrP roklaProkl aklaGluGlu thrMetThrT hrSerProGly 701 CCAGCOCGGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGG TGCTGAAGAG ACAATGACCA CCAGCCOGGG GOICGACGAC TYCTOTGITA CITOIGGICG GGTCCCIGAG GACGGGGICG ACGACTTCIC TGITACIGGI GGTCGGGGCC GGTCGGGCCC CTGAGGACGG SerProGl 171
- 16 801 GACTCCINCC CCAGCIGCIG AAGAGACAAI GACCACCAGC CCGGGGACIC CIGCCCCAGC IGCTGAAGAG ACAAIGACCA CCAGCCCGGG GACICCIGCC ITCICIGITA CIGGIGGICG GCCCCLIGAG GACGGGGICG ACGACITCIC TGILACIGGI GGICGGGCCC CICAGGACGG yThrProAla Thrproala ProalaalaG luGluThrMe tThrThrSer ProGlyThrP roalaProal aalaGluGlu ThrMetThrT hrSerProGl GGTCGACGAC CTGAGGACGG 204
 - 901 TCTICICATI ACCICICAIG CACCAICCIA GGGAICAIAG TICIAATIGI GCTICICATI GIGITIGITI GAAAGACTIC ACIGIGGAAG AAATICCITC agaagataa tggagagtac ctggtaggat ccctagtatc aagattaaca cgaagactaa cacaaacaaa cittictgaag tgacacettc tttaaggaag SerSerHisT yrLeuSerCy sThrileVal GlytleileV alLeuileVa lLeuLeuile ValPheVal
- 1001 CTROCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC AGAAACGCCT AGACGACACA AGGGTGTCTG TCTTTGCGGA GAATGGACIT TCCAAGICCA TCCGGGACCG ACTCCCGCCC CCGCGACCT GTGAGAGACG GGACGGAGGG
 - CGGGACGGG GIUTITUTT TITITITUT TITITITUT TITITITUT TITITITUT TITITITUT TITITITUT TITITITUT 1101 GCCCCIGCC Chararara arraharar araharara araharara araharara araharara araharara

FIG._ 1B-2

Apo2 Apo2DcR	1 1	meqrqqnapaasgarkrhgpgpreargarpglrvpktivt
DR4	51	GRGALPTSMGQHGPSARARAGRAPGFRPAREASPRLRVHKTFKFVVVGVL
Apo2	41 13	vvaavlilvsaesalitoodlapooraapooressesegleppeheised vivavlilviaysattaroeevpootvapooorespreeecpagserseh
Apo2DcR DR4	101	LQVVPSSAATIKTLHDQSIGTQQWEHSPLGELCPPGSHRSER
Apo2		GRDCLSCKYGQDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQCE
Apo2DcR DR4	63 142	
Apo2	141	CRD2 EGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVHKE
Apo2DcR DR4	113 192	EGTFRNENSPEMCRKCSR-CPSGEVGVSNCTSWDDIQCVE-EFGANATVE FGTFRNDNSAEMCRKCSTGCPRGMVKVKDCTPWSDTECVHKE
Apo2		
Apo2DcR DR4	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
Apo2		SGIIIGVTVAAVVLIVAVEV
Apo2DcR DR4	211 234	ETMTTSPGTPAPAAEETMTTSFGTPASSHYLSCTIVGIIVLIVLLIVFVSGNGHNIWVTLVVTLVVPILIVAV-LIVC
DR4		
Apo2 DR4	203 262	CKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP CCIGSGCGGDPKCMDRVCFWRLGLLEGPGAEDNAHNEILSNADSLSTFVS
Apo2	253	
DR4	312	EQQMESQEPADITGVTVQSPGEAQCLIGPAEAEGSQRRRLLVPANG
Apo2	303	CDPTETIROCFDDFADIVPFDSWEFINRKIGIMDNEIKVAKABAAGH - R ADPTETIMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVKAGTAGP - G
DR4 Apo3/DR3	358 338	ADPTETIMETEDARANIVPFDSWDQLMRQDDITRMETDVVRAGTAGPG VMDAVPARRWKEFVRILGLREAEIEAVEVEI-GRF-R
TNFR1	322	vvenypplrwkefyrrlgisdheidrielon grcir iagvhtlsqykgfyrkngvneakideikndn-vodta
CD95	220	THE AUTTO SAME AND AUTOM AND THE TRUTH A STOLE
Apo2	351	
DR4 Apo3/DR3	406 374	DALYAMIMKWVNKTGR-NASTHTLLDALERMEERHAKEKIQDLLVDSGKF DOQYEMIKRWRQQQPAGLGAVYAALERMGLDGCVEDLRS
TNFR1	358	EACYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEE
CD95	256	
Apo2		MYLEGNADSALS
DR4	455	IYLEDGTGSAVSLE





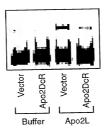


FIG._6

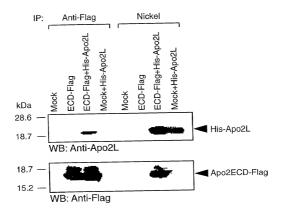
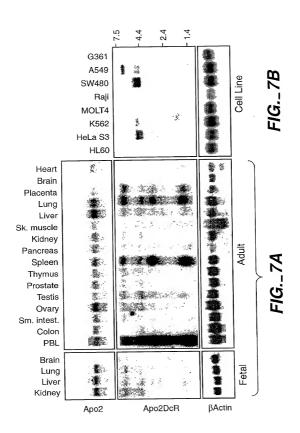


FIG._10



				>,
GGGCTGAAAC	CCCGACTTTC	CACGGCCCAG	GIGCCGGGIC	M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly
TCTACTTTAA	AGATGAAATT	CCGGAAAAGG	GGCCTTTTCC	aArgLysArg
CGATGCCCGA	GCTACGGGCT	CITCGGGGGC	GAAGCCCCCG	laserGlyAl
AATACACCGA	TTATGTGGCT	9009900009	200220000	AlaProAlaA
GCCCCCACAA	CGCGGGTGTT	GGGACAGAAC	CCCTGTCTTG	gGlyGlnAsn
CGCAATCTCT	GCGTTAGAGA	TGGAACAACG	ACCTTGTTGC	etGluGlnAr
CCCAGAACCC	GCCTCTTGGG	CCTACCGCCA	GGATGGCGGT	×
AGCACCCGCC	rcgrecece	AAGAGCGTTC	TTCTCGCAAG	
CGCATAAATC	SGETCEGCAG GCGTATTAG ICCTGCGCCG GCCTCTTGGG GCGTTAGAGA CGCGGGTGTI TTATGTGGCT GCTACGGGCT AGATGAAATI CCCGACTTTG	GAGAGACTAT	SGEGCCCGGA CECTCFGAIA TECTCGCAAG GGATGGCGGF ACCTTGTTGC CCCTGTCTTG CGGGGCCGGC GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC	
1 CCCAGGGGTC GGATAAATC AGCAGGGGG GGGAGAACGC GGGAATCTCT GGGCCCACAA AATACACGGA GGATGCGCGA TCTACTTTAA GGGCTGAAAC	GGGTGCCCAG	01 CCACGGGCCT GAGAGATAT AAGAGGGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCGGGCG CTTCGGGGGGC CCGGAAAAG CACGGCCCAG	GGTGCCCGGA	
-		0.1		Н

- ProhrgGl uhlahrgGly hlahrgProG lyLeuhrgVa lProLysThr LeuValLeuV alValhlahl aValLeuLeu LeuValSerh laGluSerhla 201 GACCCAGGA GGGGGGGGA GCCAGGCCTG GGCTCCGGGT CCCCAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTGC ctedetecct eccedeces essteceare ecardeceer aggetteteg garcaegage aacaegege ecaggagare aacaabate gaeteabaeg
- 301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGG GCCCACAAC AAAAGAGGTC CAGCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC AGACTAGTGG GITGITCTGG ATCGAGGGGT CGTCTCTCGC CGGGGTGTTG TITTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC TGTGGTATAG Leullethr GinglnAspt eualaproci nGinArgala alaprocing inLysArgse rSerproser GludlyLeuc ysproproci yHisHisIle
- 401 ICAGAAGACG GTAGAGATTG CAICTGCTGC AAATATGGAC AGGACTATAG CACTCAGG AATGACCTGC TTTTCTGCTT GGGCTGCACC AGGTGTGATT AGTCTTGTGC CATCTCTAAC GTAGAGGAGG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGAGGAA GGGGAGG TCCACACTAA

8 /

- 16 SerGluhapg lyargaspCy slleSerCys LysTyrGlyg lnaspTyrSe rThrHisTrp AsnaspLeuL euPheCysLe uArgCysThr ArgCysAspSer
 - lGluLeuSer ProCysThrT hrThrarghs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg 501 CAGGIGAAGI GGAGCIAAGI CCCIGCACCA CGACCAGAAA CACAGIGIGI CAGIGCGAAG AAGGCACCII CGGGGAAGAA GAIICICCIG AGAIGIGCG CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTCACACA GTCACGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC GTCCACTTCA GlyGluVa 122
- GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAÁTCAGG CATCATCATA CITCACGGCG IGICCCACAG GGTCICCCIA CCAGIICCAG CCACIAACAI GIGGBACCIC ACIGIAGCII ACACAGGIGI IICIIAGICC GIAGIAGIAI LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerGl yIleIlelle 155
- 188 Glyvalmhrv alhlahlava lvalLeulle Valhlavalp hevalcysty sSerLeuLeu TrpLysLysv alLeuProfy rLeuLysGly IlecysserGly 101 GENGTCACNG TIGCNGCGGT NGICTIGNII GIGGCTGIGI ITGITIGCAN GICTIINCIG IGGANGAANG ICCITICTIN CCIGAANGGC AICIGCTOG cctcrgigtc aacgtcggca icagaactaa caccaacaca aacaaaugii cagaaatgac acctictitc aggaaggaai ggaciticcg iagaaggagc

FIG._8A-1

801 GIGGIGGIGG GGACCCTGAG COTGIGGACA GGACCTCACA ACGACCTGGG CCTGAGGACA AIGICCTGAA TGAGATGGIG AGIATCTIGC AGCCCACCCA	901 GGTCCCGGGG GAGTANTGG ANGTCCAGGA GCCAGCAGAG CCAACCAGGTG TCAACATGTT GTCCCCGGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA	1001 GETANAGOT CTONANGAG GAGGCTGCTG GTTCCAGCAA ATCAAGGTGA TCCAACTGAG ACTCTGAGAC AGTGCTTGGA TGACTTTGGA GACTTGGTG
CACGACCAC CCTGGGACTC GCACACTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TGGGGTGGGT	CCAGGACTC GTCCTTTACC TTCAGGTCCT GGGTCGTTCT GGTTGTACAA CAGGGGGCCC CTCAGTCTG TAGAGAACT TAGCGGCCT	CGACTTTGCA GAGTGTGCTC CTGGGAGGAC CAAGGTGGTT TACTTCCACT AGGGTGACTC TGAGACTTGTT ACTGTAAAGGT GTGAAACGT
222 GLYGLYGL YASPPTGGLI AYGYALASPA IGSETSEFGI NAYGPYGGLY ALAGLUASPA SNVALLEUAS GALULLEVAL SETILELEUG INPICTHYGIN	CCAGGACTC GTCCTTTACC TTCAGGTCCT GGGTCGTTCT GGTTGTACAAAAAAAAAA	288 AlaGluargS exclaargar gargleuleu Valfroalaa snGluGlyas pProThrdlu ThrieuargG lnCyspheas pAspbheala AspleuValfar
AGTATCTTGC	ATCTGCTGGA	TGACTTTGCA
TCATAGAACG	TAGACGACCT	ACTGAAACGT
SerileLeuG	isLeuLeuGl	paspPheAla
TGAGATCGTG	GAGTCAGAGC	AGTGCTTCGA
ACTCTAGCAC	CTCAGTCTCG	TCACGAAGCT
nGluileVal	GluserGluH	InCysPheAs
ATGTCCTCAA	GTCCCCGGG	actctgagag
TACAGGAGTT	CAGGGGGCCC	tgagactctg
SNVAlleuAs	uSerProGly	thrleuargG
GCTGAGGACA	TCAACATGTT	TCCCACTGAG
CGACTCCTGT	AGTTGTACAA	AGGGTGACTC
AlaGluAspA	alasnMetLe	pProThrGlu
ACGACCTGGG	CCAACAGGTG	ATGAAGGTGA
TGCTGGACCC	GGTTGTCCAC	TACTTCCACT
nArgProGly	ProThrGlyV	snGluGlyAs
GAAGCTCACA	GCCAGCAGAG	GTTCCAGCAA
CTTCGAGTGT	CGGTCGTCTC	CAAGGTCGTT
rgSerSerGl	uProAlaGlu	VAlProAlaA
CGTGTGGACA	AAGTCCAGGA	GAGGCTGCTG
GCACACCTGT	TTCAGGTCCT	CTCCGACGAC
Argvalaspa	luvalGlnGl	gArgleuleu
GGACCCTGAG CCTGGGACTC yASpProGlu	CAGGAAATGG GTCCTTTACC	CTCAGAGGAG GAGTCTCCTC erGlnArgAr
GTGGTGGTGG CACCACCACC GlyGlyGl	GGTCCCTGAG CCAGGGACTC	GCTGAAAGGT CGACTTTCCA AlaGluArgS
801	901	1001

9/16

FIG._8A-2

HODDIAG: A/A/AAAG

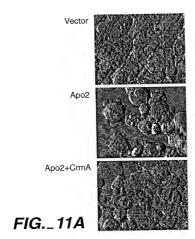
CONTROLL STATEMENT OF THE CACADADA GACADADAGE TEREGERACE GECCACAGE ACACCITYTA	1101 CENTIFICACIC CIGGAGCCG CICATGAGGA AGIILGGCCI CAIGGAGGGG CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR TGTGGAACAT	100000000000000000000000000000000000000	GGAACIGAG GACCCICGGG GAGIACICCI ICMICCCITIC COMPANIA COMPANIA ACTICATOR ACTICATOR GOVERNATOR GIVERSARGA SPINIFICATIVE	
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TARCASSTAC	*****************	GIACCIGITA		UMETASDASI
m 0000000	100001108	TO DO DO G G G A		all of all all a
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	CIGGGAGGGG	000000000000000000000000000000000000000	GACCCITCGGC	
	COMPTGACTC		GGAAACTGAG	
	1101	4		

- ThrMetLeu IleLysTrpV alAsnLysTh rClyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln 1201 CACCATECTS ATARACTESS TCARCARARA CESSESAGAT SECTETSTEC ACACCETSCT SSATGCETTS SAGACSTES SAGAGACAT TSCCAASCAG GIGCIACGAC TATITCACC AGTIGITITG GCCCGCICIA CGGAGACAGG IGIGGGACGA CCIACGGAAC CICIGGGGAC CICICICIGA ACGCITUGIC Pheaspse rirpgiurro reumedargu ysa
- 1101 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGITCATGT AICTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG AITCTCTTCA GGAAGTGAGA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAAC TAAGAGAAGT CCTTCACTCT 188 Lysileciun spHisLeule uSerSercly LysPheHetT yrLeucluci yAsnalaAsp SerAlaXqqS erOC* TGGTGAACAA TTCTAACTCC
- 10 TITACCTITI ITCIGGAAAA AGCCCAACIG GACICCAGIC AGIAGGAAAG IGCCACAAIT GICACAIGAC GGGIACIGGA AGAAACICIC TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG AAATGGAAAA AAGACCTTTT 1401 CCTICCCIGG
- 16 CCHICCAACA TCACCCAGIG GAIGGAACAT CCIGIAACIT ITCACIGCAC IIGGCATIAT ITTIAIAACC IGAAIGIGAT AAIAAGGACA CIAIGGAAAT GGINGGITGI NGIGGGICNC CINCCIIGIN GGNCAITGNA ANGIGNCGIG ANCCGINAIN AAAAINIICG NCIINCACIA ITAIICCIGI GAIACCIITA
 - GTOTGGATCA TICCGTITGI GCGIACTITG AGAITIGGII IGGGAIGTCA TIGTITITCAC AGCACTITIT TAICCIAAIG DAAAIGCITI AITTAITHAI Chgricthgt anggcarach cgchtgaarc tctrarccar accctrcrgf arcarargt tcgtgarara atrogattrc atttrcgara 1601
 - AACCGANGT AACAFTCIAG GIAGATGFFF TETFFFFFFF TTFFFFFF CCGCCGCCG TGAGATGFCA GCTCGAGGFC TECGAACGG CGGFACGG 1701 TTGGGCTACA TIGIRAGAIC CAICTACAAA AAAAAAAAA AAAAAAAAA GGGGGCGGG ACICIAGAGI GGACCIGGAG AAGCTIGGGC

FIG._8B

LAPQQRAAPOQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDXSTHWNDILFCLRCTRCD SGEVELSPCTTRNIVVCQCEEGTFREEDSPERCRRCRTGCPRGWKVGDCTPWSDIRCVH NEGDPTETLROCFDDFADLVPFDSWEPLARKIGLMDNEIKVARAEAAGHEDTLYTMLLKM VNKTGRDASVFTLLDALETLGERLAKOKIEDHLLSSGKFWYLEGNADSALS KESGIIIGVTVAAVVLTVAVFVCKSLLMKKVLPYLKGICSGGGDPERVDRSSQRPGAED NVINEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPPA MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVVVAAVLLLVSAESALITQQD 181 241 121 301 61

FIG._9



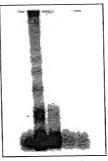
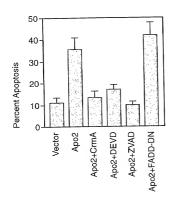


FIG._11B

Apo2 Apo2+CrmA Apo2+DEVD Apo2+ZVAD



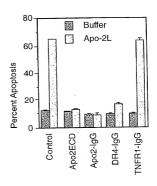
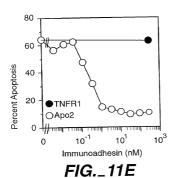


FIG._11C

FIG._11D



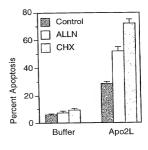
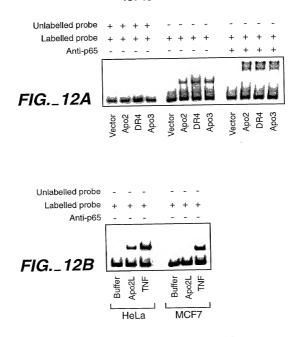
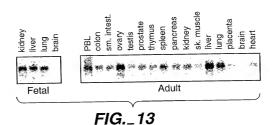
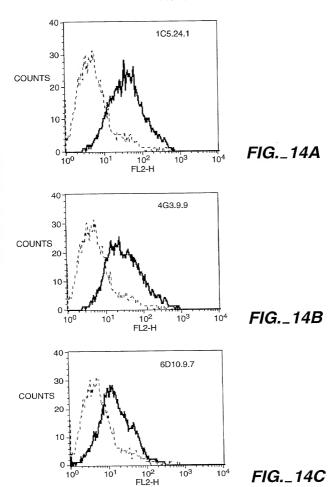


FIG._12C







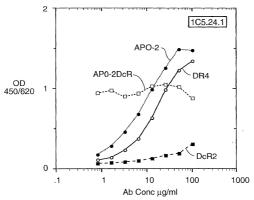


FIG._15A

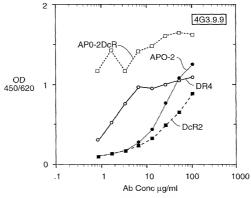
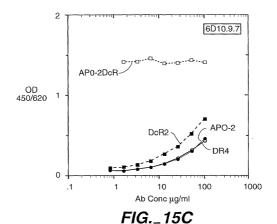


FIG._15B



Summary of mAbs to DcR1

mAbs	ISOTYPE	FACS Cross reactivity				
		(HUMEC)	DR4	Apo-2	Apo-2DcR	DcR2
1C5.24.1	IgG1	+	++	+++	+++	-
4G3.9.9	IgG1	+	++	+	+++	+/-
6D10.9.7	IgG2b	+	-	-	+++	+/-

Percent Cross reactivity was determined by comparing the binding capacity to Apo-2DcR at 10 ug/ml of mAbs in ELISA. ++: >75% , +: 25-75%, +/-:10-25%, -: <10% .

FIG._16